

#2

OPIPE

**RAW SEQUENCE LISTING**

DATE: 07/05/2001  
TIME: 11:25:37

Input Set : A:\003592-007.ST25.txt  
Output Set: N:\CRF3\07052001\I882774.raw

4 <110> APPLICANT: Houston, Michael E.  
5 Hodges, Robert  
7 <120> TITLE OF INVENTION: Use of Coiled-Coil Structural Scaffold to Generate  
8 Structure-Specific Peptides  
10 <130> FILE REFERENCE: 003592-007  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/882,774  
C--> 12 <141> CURRENT FILING DATE: 2001-06-14  
12 <150> PRIOR APPLICATION NUMBER: US 60/211,892  
13 <151> PRIOR FILING DATE: 2000-06-14  
15 <150> PRIOR APPLICATION NUMBER: US 60/213,387  
16 <151> PRIOR FILING DATE: 2000-06-23  
18 <160> NUMBER OF SEQ ID NOS: 16  
20 <170> SOFTWARE: PatentIn version 3.0  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 619  
24 <212> TYPE: PRT  
25 <213> ORGANISM: Streptococcus pneumoniae  
27 <400> SEQUENCE: 1  
29 Met Asn Lys Lys Lys Met Ile Leu Thr Ser Leu Ala Ser Val Ala Ile  
30 1 5 10 15  
32 Leu Gly Ala Gly Phe Val Ala Ser Gln Pro Thr Val Val Arg Ala Glu  
33 20 25 30  
35 Glu Ser Pro Val Ala Ser Gln Ser Lys Ala Glu Lys Asp Tyr Asp Ala  
36 35 40 45  
38 Ala Lys Lys Asp Ala Lys Asn Ala Lys Lys Ala Val Glu Asp Ala Gln  
39 50 55 60  
41 Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu Asp  
42 65 70 75 80  
44 Gln Lys Lys Thr Glu Glu Lys Ala Ala Leu Glu Lys Ala Ala Ser Glu  
45 85 90 95  
47 Glu Met Asp Lys Ala Val Ala Ala Val Gln Gln Ala Tyr Leu Ala Tyr  
48 100 105 110  
50 Gln Gln Ala Thr Asp Lys Ala Ala Lys Asp Ala Ala Asp Lys Met Ile  
51 115 120 125  
53 Asp Glu Ala Lys Lys Arg Glu Glu Ala Lys Thr Lys Phe Asn Thr  
54 130 135 140  
56 Val Arg Ala Met Val Val Pro Glu Pro Glu Gln Leu Ala Glu Thr Lys  
57 145 150 155 160  
59 Lys Lys Ser Glu Glu Ala Lys Gln Lys Ala Pro Glu Leu Thr Lys Lys  
60 165 170 175  
62 Leu Glu Glu Ala Lys Ala Lys Leu Glu Glu Ala Glu Lys Lys Ala Thr  
63 180 185 190  
65 Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Val Ala Pro Gln Ala Lys  
66 195 200 205  
68 Ile Ala Glu Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu Lys  
69 210 215 220  
71 Glu Ile Asp Glu Ser Glu Ser Glu Asp Tyr Ala Lys Glu Gly Phe Arg

ENTER  
See page 5

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Input Set : A:\003592-007.ST25.txt  
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72	225	230	235	240
74	Ala Pro Leu Gln Ser Lys Leu Asp Ala Lys Lys Ala Lys Leu Ser Lys			
75	245	250	255	
77	Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala Glu Ile Ala			
78	260	265	270	
80	Lys Leu Glu Asp Gln Leu Lys Ala Ala Glu Glu Asn Asn Val Glu			
81	275	280	285	
83	Asp Tyr Phe Lys Glu Gly Leu Glu Lys Thr Ile Ala Ala Lys Lys Ala			
84	290	295	300	
86	Glu Leu Glu Lys Thr Glu Ala Asp Leu Lys Lys Ala Val Asn Glu Pro			
87	305	310	315	320
89	Glu Lys Pro Ala Pro Ala Pro Glu Thr Pro Ala Pro Glu Ala Pro Ala			
90	325	330	335	
92	Glu Gln Pro Lys Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro Lys			
93	340	345	350	
95	Pro Glu Lys Pro Ala Glu Gln Pro Lys Pro Glu Lys Thr Asp Asp Gln			
96	355	360	365	
98	Gln Ala Glu Glu Asp Tyr Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg			
99	370	375	380	
101	Leu Thr Gln Gln Gln Pro Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro			
102	385	390	395	400
104	Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr			
105	405	410	415	
107	Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp Tyr			
108	420	425	430	
110	Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn			
111	435	440	445	
113	Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp			
114	450	455	460	
116	Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met			
117	465	470	475	480
119	Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala			
120	485	490	495	
122	Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr			
123	500	505	510	
125	Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn			
126	515	520	525	
128	Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp			
129	530	535	540	
131	Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met			
132	545	550	555	560
134	Ala Thr Gly Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala			
135	565	570	575	
137	Ser Gly Ala Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp			
138	580	585	590	
140	Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala Val Asn Thr Thr Val Asp			
141	595	600	605	
143	Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp Val			
144	610	615		

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Input Set : A:\003592-007.ST25.txt  
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147 <210> SEQ ID NO: 2  
 148 <211> LENGTH: 40  
 149 <212> TYPE: PRT  
 150 <213> ORGANISM: Artificial Sequence  
 152 <220> FEATURE:  
 153 <223> OTHER INFORMATION: stabilizing strand  
 155 <220> FEATURE:  
 156 <221> NAME/KEY: MOD\_RES  
 157 <222> LOCATION: (2)  
 158 <223> OTHER INFORMATION: Nle  
 160 <400> SEQUENCE: 2  
 W--> 162 Cys Xaa Gly Gly Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala  
       1              5                 10                         15  
 163 Leu Lys Lys Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala Leu Lys  
       20                 25                         30  
 165 Lys Glu Ile Glu Ala Leu Lys Lys  
 166                 35                        40  
 168 Lys Glu Ile Glu Ala Leu Lys Lys  
 169                 35                        40  
 171 <210> SEQ ID NO: 3  
 172 <211> LENGTH: 38  
 173 <212> TYPE: PRT  
 174 <213> ORGANISM: Artificial Sequence  
 176 <220> FEATURE:  
 177 <223> OTHER INFORMATION: hybrid sequence  
 179 <220> FEATURE:  
 180 <221> NAME/KEY: MOD\_RES  
 181 <222> LOCATION: (2)  
 182 <223> OTHER INFORMATION: Nle  
 184 <400> SEQUENCE: 3  
 W--> 186 Cys Xaa Gly Ile Glu Glu Leu Glu Lys Lys Ile Thr Glu Leu Lys Gln  
       1              5                 10                 15  
 187 Lys Ile Asp Ala Leu Glu Asn Gln Ile His Arg Leu Glu Gln Glu Ile  
       20                 25                         30  
 189 Lys Glu Leu Asp Glu Ser  
 190                 35  
 192 Lys Glu Leu Asp Glu Ser  
 193                 35  
 195 <210> SEQ ID NO: 4  
 196 <211> LENGTH: 38  
 197 <212> TYPE: PRT  
 198 <213> ORGANISM: Artificial Sequence  
 200 <220> FEATURE:  
 201 <223> OTHER INFORMATION: hybrid sequence  
 203 <220> FEATURE:  
 204 <221> NAME/KEY: MOD\_RES  
 205 <222> LOCATION: (2)  
 206 <223> OTHER INFORMATION: Nle  
 208 <400> SEQUENCE: 4  
 W--> 210 Cys Xaa Gly Leu Glu Glu Ala Glu Lys Lys Ala Thr Glu Ala Lys Gln  
       1              5                 10                 15  
 211 Lys Val Asp Ala Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu  
       20                 25                         30  
 213

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Input Set : A:\003592-007.ST25.txt  
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216 Lys Glu Ile Asp Glu Ser  
217 35  
219 <210> SEQ ID NO: 5  
220 <211> LENGTH: 20  
221 <212> TYPE: PRT  
222 <213> ORGANISM: Artificial Sequence  
224 <220> FEATURE:  
225 <223> OTHER INFORMATION: consensus sequence  
227 <220> FEATURE:  
228 <221> NAME/KEY: PEPTIDE  
229 <222> LOCATION: (4)..(20)  
230 <223> OTHER INFORMATION: Amino acids 4, 5, 12, 16 and 20 are Xaa wherein Xaa = any amino

231 acid  
233 <400> SEQUENCE: 5  
W--> 235 Glu Glu Leu Xaa Xaa Lys Ile Asp Glu Leu Asp Xaa Glu Ile Ala Xaa  
236 1 5 10 15

W--> 238 Leu Glu Lys Xaa  
239 20  
241 <210> SEQ ID NO: 6  
242 <211> LENGTH: 8  
243 <212> TYPE: PRT  
244 <213> ORGANISM: Artificial Sequence  
246 <220> FEATURE:  
247 <223> OTHER INFORMATION: consensus sequence

249 <400> SEQUENCE: 6  
251 Glu Glu Leu Ser Asp Lys Ile Asp  
252 1 5  
254 <210> SEQ ID NO: 7  
255 <211> LENGTH: 27  
256 <212> TYPE: PRT  
257 <213> ORGANISM: Artificial Sequence  
259 <220> FEATURE:  
260 <223> OTHER INFORMATION: hybrid sequence

262 <220> FEATURE:  
263 <221> NAME/KEY: MOD\_RES  
264 <222> LOCATION: (2)  
265 <223> OTHER INFORMATION: Nle  
267 <400> SEQUENCE: 7

W--> 269 Cys Xaa Gly Glu Ile Glu Ala Leu Lys Lys Lys Ile Glu Glu Leu Ser  
270 1 5 10 15

272 Asp Lys Ile Asp Glu Leu Glu Lys Glu Ile Lys  
273 20 25

275 <210> SEQ ID NO: 8  
276 <211> LENGTH: 21  
277 <212> TYPE: PRT  
278 <213> ORGANISM: Haemophilus influenzae

280 <400> SEQUENCE: 8  
282 Ile Lys Lys Val Leu Glu Ile Gly Leu Asn Met Ser Gln Glu Ala Ser  
283 1 5 10 15

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```

285 Asn Leu Thr Ser Ala
286          20
288 <210> SEQ ID NO: 9
289 <211> LENGTH: 27
290 <212> TYPE: PRT
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: hybrid sequence
296 <400> SEQUENCE: 9
298 Glu Ala Glu Ile Lys Lys Leu Leu Glu Ile Ile Leu Asn Leu Ser Gln
299 1           5           10           15
301 Glu Ile Ser Asn Leu Thr Ser Ala Leu Lys Gly
302          20           25
304 <210> SEQ ID NO: 10
305 <211> LENGTH: 20
306 <212> TYPE: PRT
307 <213> ORGANISM: Streptococcus pneumoniae
309 <400> SEQUENCE: 10
311 Leu Glu Lys Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Gln Ala
312 1           5           10           15
314 Glu Gln Val Leu
315          20
317 <210> SEQ ID NO: 11
318 <211> LENGTH: 15
319 <212> TYPE: PRT
320 <213> ORGANISM: Streptococcus pneumoniae
322 <400> SEQUENCE: 11
324 Leu Glu Asp Asn Leu Lys Asp Ala Glu Thr Asn Asn Val Glu Asp
325 1           5           10           15
327 <210> SEQ ID NO: 12
328 <211> LENGTH: 10
329 <212> TYPE: PRT
330 <213> ORGANISM: Streptococcus pneumoniae
332 <400> SEQUENCE: 12
334 Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys
335 1           5           10
337 <210> SEQ ID NO: 13
338 <211> LENGTH: 35
339 <212> TYPE: PRT
340 <213> ORGANISM: Artificial Sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: hybrid sequence
345 <400> SEQUENCE: 13
347 Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Leu Glu Asp Asn Leu
348 1           5           10           15
350 Lys Asp Ala Glu Thr Asn Asn Val Glu Asp Ala Lys Lys Gln Thr Glu
351          20           25           30
353 Leu Glu Lys
354          35

```

FYF

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

**VERIFICATION SUMMARY**

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Input Set : A:\003592-007.ST25.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16